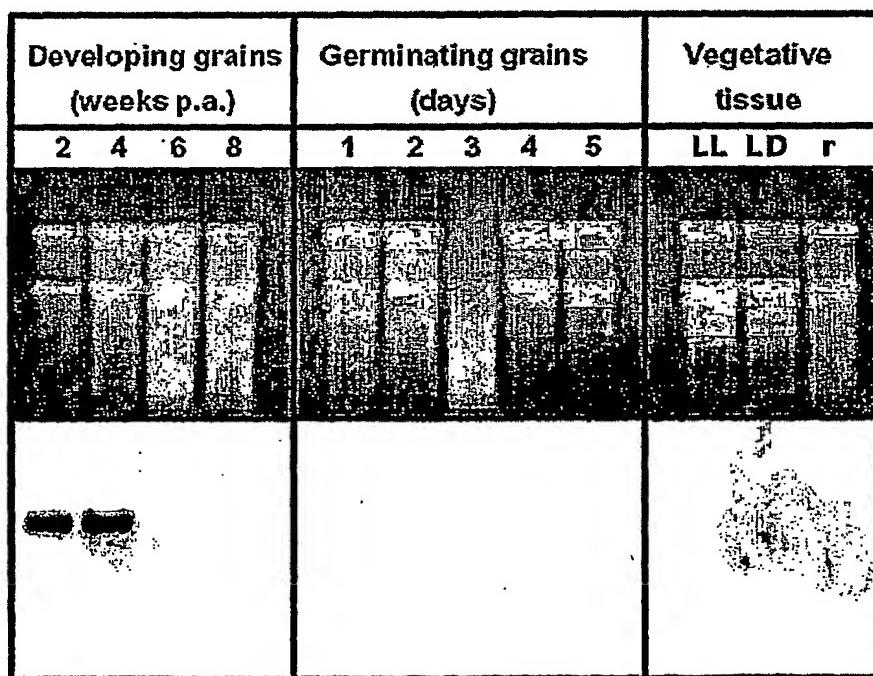


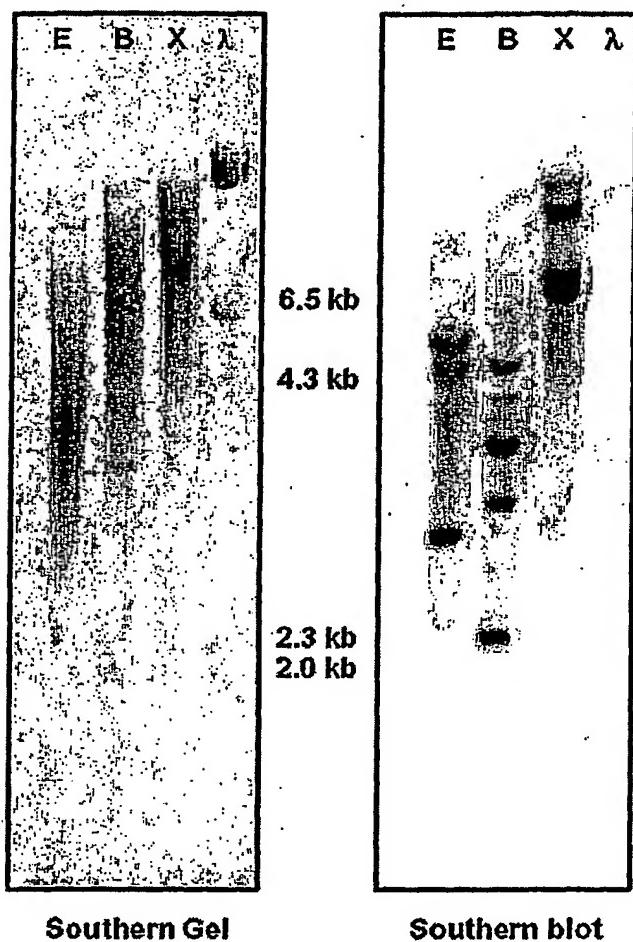
Figure 1. RT-PCR analysis of barley limit dextrinase inhibitor expression.

Figure 2. Northern blot analysis of limit dextrinase expression.



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Figure 3. Southern blot analysis of limit dextrinase inhibitor in barley genomic DNA.



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Figure 4. Isolation of limit dextrinase inhibitor promoter fragments by genome walking PCR.

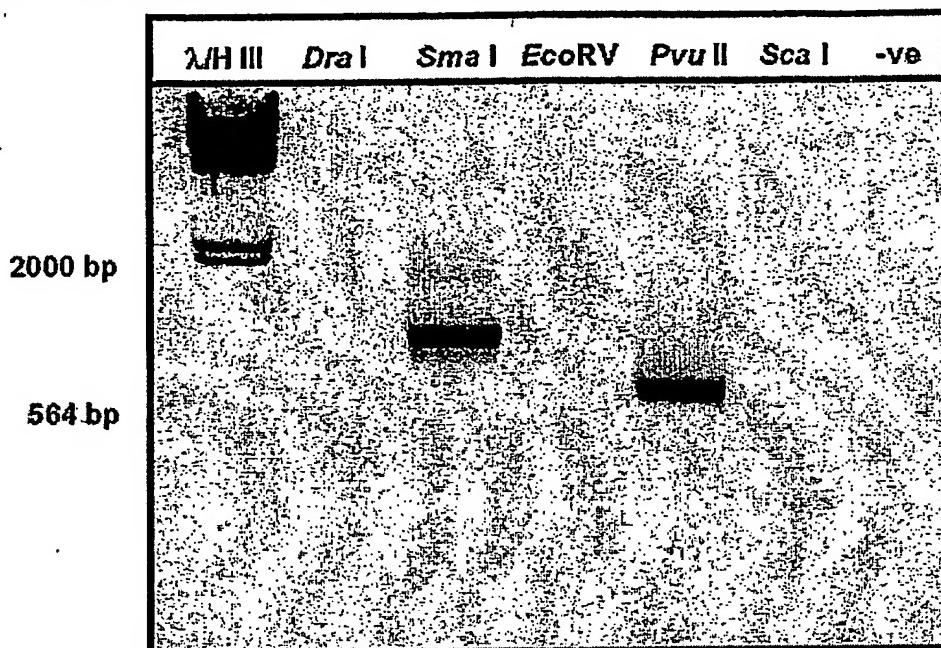
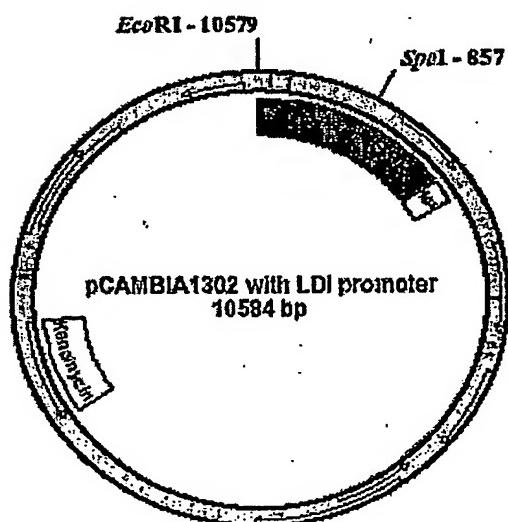
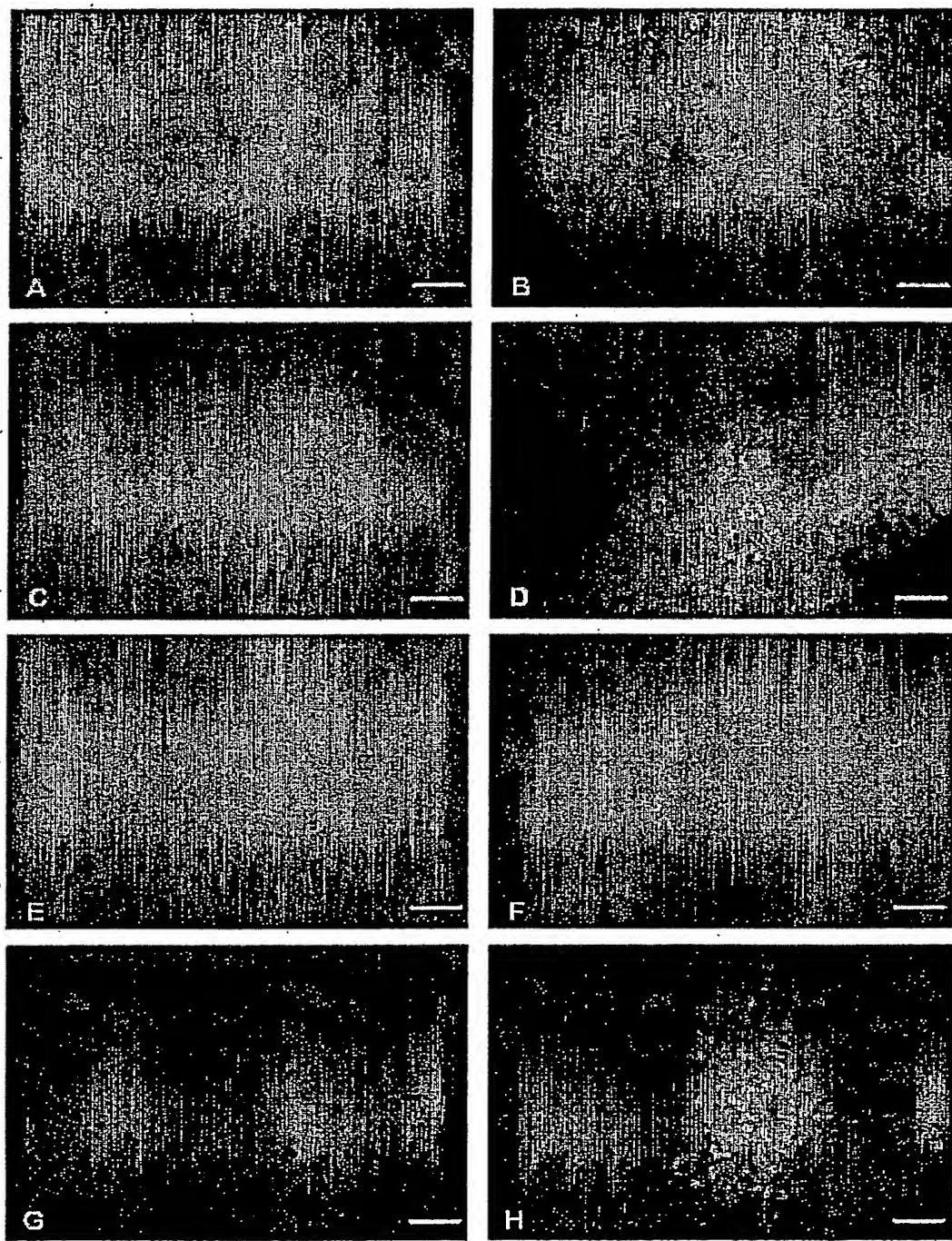


Figure 5. Barley transformation construct containing the limit dextrinase inhibitor promoter.



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Figure 6. Transient expression assays using the limit dextrinase promoter: GFP construct.



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Figure 7.

Start	End	Score	Promoter Sequence
247	297	0.89	ATGCCCGTGTAAAAGAAACCCCTTCTTCCTAAAAATATA A TATCATCGT
273	323	0.95	TTTCCTAAAAATATATATCATCGTCCGTATGATAACGTTT A TGTATTCAA
652	702	0.83	CAAGAACCTCCAAATAAACGCCAACAGAAAGAAATGAGC A TTACTTGCG

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Figure 8

Sequences producing significant alignments:	Score	E
	(bits)	Value
gi 18868 emb X13443.1 HVAATI Barley mRNA for alpha-amylase/...	82	2e-12
gi 22035404 gb AY124482.1 Danio rerio myogenin gene, exons...	80	6e-12
gi 24614584 gb AY050653.1 Giardia intestinalis SEC24 (SEC2...	76	1e-10
gi 10938038 gb AF162890.1 AF162890S1 Mus musculus peroxisom...	76	1e-10
gi 5821237 dbj AB021922.1 Homo sapiens gene for lectin-lik...	76	1e-10
gi 3721562 dbj AB011276.1 Mus musculus gene for alphala ca...	74	4e-10
gi 30313388 gb AY099112.1 Rattus norvegicus obese protein ...	72	2e-09
gi 18140057 gb AF457660.1 Castanea dentata clone ACS2 vasc...	72	2e-09
gi 4104807 gb AF039526.1 AF039526 Homo sapiens MHC class I ...	72	2e-09
gi 8050595 gb AF233737.1 AF233737 Agrotis ipsilon AiC5 chym...	72	2e-09
gi 6690643 gb AF191544.1 AF191544 Homo sapiens estrogen rec...	72	2e-09
gi 6164589 gb AF051769.1 AF051769 Homo sapiens hyaluronidas...	72	2e-09
gi 3643823 gb AF075270.1 AF075270 Hordeum vulgare high affi...	72	2e-09
gi 19919401 gb AF435445.1 Pleurotus ostreatus manganese pe...	70	6e-09
gi 8132114 gb AF153014.1 Trichomonas vaginalis Tvp14 (tvp1...	70	6e-09
gi 4456992 gb AF077743.1 AF077743 Mus musculus transcriptio...	70	6e-09
gi 12276207 gb AF269146.1 AF269146 Bilophila wadsworthia ta...	70	6e-09
gi 14275833 emb AJ289605.1 MMU289605 Mus musculus partial L...	70	6e-09
gi 3378604 emb AJ009889.1 HSAJ9889 Homo sapiens GHR gene, V...	70	6e-09
gi 3916231 gb AF074397.1 AF074397 Homo sapiens anti-mulleri...	70	6e-09
gi 5139506 emb Z18892.2 MMDESMINP Mus musculus desmin gene	70	6e-09
gi 15487305 dbj AB060299.1 Mus musculus gene for acetyl Co...	70	6e-09
gi 12697590 dbj AB046716.1 Homo sapiens hST3Gal I gene for...	70	6e-09
gi 25453365 gb AY050651.2 Giardia intestinalis MYB (MYB) m...	68	2e-08
gi 13183059 gb AF237414.1 Anaplasma phagocytophilum RNA po...	68	2e-08
gi 13625520 gb AY014277.1 Lolium perenne gibberellin 20-ox...	68	2e-08
gi 17105179 gb AF439558.1 AF439558 Mus musculus X2CR1 gene,...	68	2e-08
gi 16209547 gb AY052528.1 Glycine max calmodulin isoform-4...	68	2e-08
gi 15213480 gb AF241535.1 AF241535 Homo sapiens mucin 4 (MU...	68	2e-08
gi 15558849 emb AJ310936.1 FSO310936 Fusarium solani chy ge...	68	2e-08
gi 4878023 gb AF131239.2 AF131239 Rattus norvegicus alpha 1...	68	2e-08
gi 15216031 emb AJ318812.1 VFA318812 Vicia faba var. minor ...	68	2e-08
gi 4454294 emb AJ132779.1 MMU132779 Mus musculus p107 gene ...	68	2e-08
gi 3133088 emb Y16736.1 HSA16736 Homo sapiens dif-2 gene, p...	68	2e-08
gi 6690521 gb AF154245.1 AF154245 Rattus norvegicus chemota...	68	2e-08
gi 5731977 gb AF114032.1 AF114032 Mus musculus glycogenin-1...	68	2e-08
gi 26453412 dbj AB094665.1 Seriola quinqueradiata YGHL1 ge...	68	2e-08
gi 4039145 gb AF099083.1 AF099083 Homo sapiens growth hormo...	68	2e-08
gi 2739123 gb AF029214.1 MMOX2S1 Mus musculus MRC OX-2 anti...	68	2e-08
gi 2895903 gb AF046916.1 AF046916 Ruminococcus flavefaciens...	68	2e-08
gi 1916583 gb U53907.1 RNU53907 Rattus norvegicus microsat...	68	2e-08

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gi 6683556 gb AB024534.1	Rattus norvegicus gene for thiaz...	68	2e-08
gi 7109286 gb AF227508.1	Rattus norvegicus intestinal alka...	66	1e-07
gi 13345792 gb AF332759.1	Homo sapiens partially duplicate...	66	1e-07
gi 5002511 emb Z98266.1 HSZ98266	Homo sapiens gene encoding...	66	1e-07
gi 6560627 gb AF112228.1 HSCD30P1	Homo sapiens CD30 protein...	66	1e-07
gi 24475537 gb AB084484.1	Betula platyphylla DNA, microsa...	66	1e-07
gi 28875405 gb AF515463.1	Biomphalaria glabrata fibrinogen...	64	4e-07
gi 18140058 gb AF457661.1	Castanea dentata clone ACS10A va...	64	4e-07
gi 2581766 gb U77633.1 RNU77633	Rattus norvegicus chromosom...	64	4e-07
gi 2764739 emb AJ002743.1 HSAJ2743	Homo sapiens cardiotroph...	64	4e-07
gi 7579914 emb AJ277249.1 HSA277249	Homo sapiens partial HR...	64	4e-07
gi 1518845 gb U63899.1 MMU63899	Mus musculus Girk2 gene, pr...	64	4e-07
gi 7109284 gb AF227507.1	Rattus norvegicus intestinal alka...	62	2e-06
gi 12744733 gb AF318503.1	Danio rerio Myod (myod) gene, co...	60	6e-06
gi 2581767 gb U77634.1 RNU77634	Rattus norvegicus chromosom...	60	6e-06
gi 14251200 gb AF220499.2 AF220499	Acidithiobacillus ferroo...	60	6e-06
gi 14043019 gb AF221946.2 AF221946	Rickettsia rickettsii ce...	60	6e-06
gi 2342636 emb Y11638.1 MMY11638	M.musculus CYP4A14 gene, e...	60	6e-06
gi 18873678 emb AJ272507.1 HSA272507	Homo sapiens partial K...	60	6e-06
gi 2564335 gb AB008218.1 AB008218S1	Homo sapiens gene for ...	60	6e-06
gi 17907575 emb AJ409277.1 CDR409277	Camelus dromedarius pa...	58	2e-05
gi 5091690 gb AF139181.1 AF139181	Bartonella henselae S-ade...	58	2e-05
gi 14164368 gb AB052355.1 AB05234S16	Mus musculus gene for...	58	2e-05
gi 15081477 gb AF401090.1	Wolbachia pipiens RNA polymera...	56	9e-05
gi 17298240 gb AF283339.1 F283327S13	Homo sapiens candidate...	56	9e-05
gi 4139055 gb AF072833.1 AF072833	Homo sapiens SP23 gene, p...	56	9e-05
gi 17298258 gb AF283357.1 F283327S31	Homo sapiens candidate...	54	4e-04
gi 18413572 emb AJ428930.1 XLA428930	Xenopus laevis partial...	54	4e-04
gi 18873687 emb AJ272516.1 HSA272516	Homo sapiens partial K...	54	4e-04
gi 29648446 gb AY190007.1	Pan paniscus clone BoE26-M13R LI...	52	0.001
gi 22651882 gb AF291761.1	Ipomoea batatas S-adenosylmethio...	52	0.001
gi 22347797 gb AF532732.1	Danio rerio mx gene, promoter se...	52	0.001
gi 11230634 emb AJ289159.1 HSA289159	Homo sapiens CD30 gene...	52	0.001
gi 3342093 gb AF074905.1 HOMOSLC04	Homo sapiens neuronal an...	50	0.006
gi 13377504 gb AF325198.1 AF325198	Triticum aestivum LRR14 ...	48	0.023
gi 6649909 gb AF026274.1 AF026274	Mus musculus Sumiko (sumi...	48	0.023
gi 6224791 gb AF190816.1 AF190816	Homo sapiens complement f...	48	0.023
gi 4104439 gb AF035664.1 HSTGFRB13	Homo sapiens transformin...	48	0.023
gi 21213045 emb AJ487974.1 EAM487974	Enterobacter amnigenus...	48	0.023
gi 15638904 gb AC024246.8	Homo sapiens BAC clone RP11-643O...	46	0.090
gi 15638822 gb AC079120.6	Homo sapiens BAC clone RP11-345M...	46	0.090
gi 13793999 gb AY029002.1	Pinus taeda isolate PTLTP3-iii27...	46	0.090
gi 11093799 gb AF285184.1 AF285184	Mus musculus basic trans...	46	0.090
gi 2984654 gb AF039088.1 AF039088	Homo sapiens non-hepatic ...	46	0.090
gi 3342092 gb AF074904.1 HOMOSLC03	Homo sapiens neuronal an...	44	0.36
gi 29029467 gb AY173030.1	Danio rerio zinc finger transcri...	44	0.36

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gi 2281684 gb AF009433.1	AH006708S06	Homo sapiens clone 22 ...	<u>44</u>	0.36
gi 13936217 gb AY029021.1	Pinus radiata isolate PRLTP3-iii...	<u>44</u>	0.36	
gi 13936206 gb AY029014.1	Pinus taeda isolate PTLTP9-iiii15...	<u>44</u>	0.36	
gi 13936204 gb AY029013.1	Pinus taeda isolate PTLTP4-i360 ...	<u>44</u>	0.36	
gi 13794006 gb AY029007.1	Pinus taeda isolate PTLTP3-v94 n...	<u>44</u>	0.36	
gi 13794003 gb AY029005.1	Pinus taeda isolate PTLTP6-i425 ...	<u>44</u>	0.36	
gi 24210408 emb AJ320160.1	FNU320160 Fusobacterium nucleatu...	<u>44</u>	0.36	
gi 13928026 emb AL121594.6	CNS01DRY Human chromosome 14 DNA...	<u>44</u>	0.36	
gi 8191116 gb AC040163.3	AC040163 Homo sapiens chromosome 1...	<u>44</u>	0.36	
gi 6707080 gb AF139182.1	AF139182 Bartonella henselae filam...	<u>44</u>	0.36	
gi 4028938 gb AC004230.1	AC004230 Homo sapiens Chromosome 1...	<u>44</u>	0.36	
gi 21623971 dbj AP001094.6	Homo sapiens genomic DNA, chrom...	<u>44</u>	0.36	
gi 19879812 dbj AP001363.4	Homo sapiens genomic DNA, chrom...	<u>44</u>	0.36	

Alignments

>gi|18868|emb|X13443.1|HVAATTI Barley mRNA for alpha-amylase/trypsin inhibitor
Length = 672
Score = 81.8 bits (41), Expect = 2e-12
Identities = 41/41 (100%)
Strand = Plus / Plus

Query: 793 aagagattgaaccaacgaccaataaactagtatcaacaatg 833
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 1 aagagattgaaccaacgaccaataaactagtatcaacaatg 41

>gi|22035404|gb|AY124482.1| Danio rerio myogenin gene, exons 1, 2 and 3 and complete cds
Length = 4260
Score = 79.8 bits (40), Expect = 6e-12
Identities = 40/40 (100%)
Strand = Plus / Minus

Query: 3 tcgattactatagggcacgcgtggtcgacggcccccggctg 42
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 4246 tcgattactatagggcacgcgtggtcgacggcccccggctg 4207.

>gi|24614584|gb|AY050653.1| Giardia intestinalis SEC24 (SEC24) mRNA, complete cds
Length = 1420
Score = 75.8 bits (38), Expect = 1e-10
Identities = 38/38 (100%)
Strand = Plus / Minus

Query: 5 gattactatagggcacgcgtggtcgacggcccccggctg 42
||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 1417 gattactatagggcacgcgtggtcgacggcccccggctg 1380

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Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Plus

Query: 9 actataggcacgcgtggtcgacggccggcgtg 42
||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 23 actataggcacgcgtggtcgacggccggcgtg 56

>gi|10938038|gb|AF162890.1|AF162890S1 Mus musculus peroxisomal assembly protein PEX3P (Pex3) gene, promoter and exon 1 Length = 2785

Score = 75.8 bits (38), Expect = 1e-10
Identities = 38/38 (100%)
Strand = Plus / Plus

Query: 5 gattactataggcacgcgtggtcgacggccggcgtg 42
||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 13 gattactataggcacgcgtggtcgacggccggcgtg 50

>gi|5821237|dbj|AB021922.1| Homo sapiens gene for lectin-like oxidized LDL receptor, promoter region Length = 2463

Score = 75.8 bits (38), Expect = 1e-10
Identities = 38/38 (100%)
Strand = Plus / Plus

Query: 5 gattactataggcacgcgtggtcgacggccggcgtg 42
||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 13 gattactataggcacgcgtggtcgacggccggcgtg 50

>gi|3721562|dbj|AB011276.1| Mus musculus gene for alpha1a calcium channel, partial cds Length = 2099

Score = 73.8 bits (37), Expect = 4e-10
Identities = 40/41 (97%)
Strand = Plus / Plus

Query: 9 actataggcacgcgtggtcgacggccggcgttattgg 49
||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 1 actataaggcacgcgtggtcgacggccggcgttattgg 41

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>gi|30313388|gb|AY099112.1| Rattus norvegicus obese protein gene, 5' flanking region and partial cds
Length = 1127

Score = 71.9 bits (36), Expect = 2e-09
Identities = 36/36 (100%)
Strand = Plus / Plus

Query: 7 ttactataggcacgcgtggtcgacggcccccggctg 42
|||||||
Sbjct: 17 ttactataggcacgcgtggtcgacggcccccggctg 52

>gi|18140057|gb|AF457660.1| Castanea dentata clone ACS2 vascular protein gene, promoter region
Length = 685

Score = 71.9 bits (36), Expect = 2e-09
Identities = 36/36 (100%)
Strand = Plus / Plus

Query: 7 ttactataggcacgcgtggtcgacggcccccggctg 42
|||||||
Sbjct: 9 ttactataggcacgcgtggtcgacggcccccggctg 44

>gi|4104807|gb|AF039526.1|AF039526 Homo sapiens MHC class I related protein 1 (MR1) gene, partial
cds
Length = 1423

Score = 71.9 bits (36), Expect = 2e-09
Identities = 36/36 (100%)
Strand = Plus / Plus

Query: 7 ttactataggcacgcgtggtcgacggcccccggctg 42
|||||||
Sbjct: 4 ttactataggcacgcgtggtcgacggcccccggctg 39

>gi|8050595|gb|AF233737.1|AF233737 Agrotis ipsilon AiC5 chymotrypsinogen gene, promoter region
Length = 951

Score = 71.9 bits (36), Expect = 2e-09
Identities = 36/36 (100%)
Strand = Plus / Plus

Query: 7 ttactataggcacgcgtggtcgacggcccccggctg 42
|||||||
Sbjct: 11 ttactataggcacgcgtggtcgacggcccccggctg 46

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>gi|6690643|gb|AF191544.1|AF191544 Homo sapiens estrogen receptor beta gene, promoter region and partial cds
Length = 2495

Score = 71.9 bits (36), Expect = 2e-09
Identities = 39/40 (97%)
Strand = Plus / Plus

Query: 9 actataggcacgcgtggtcacggcccccggctgttattg 48
||||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 1 actataaggcacgcgtggtcacggcccccggctgttattg 40

>gi|6164589|gb|AF051769.1|AF051769 Homo sapiens hyaluronidase-like pseudogene 1 (HYALP1), partial sequence
Length = 11957

Score = 71.9 bits (36), Expect = 2e-09
Identities = 36/36 (100%)
Strand = Plus / Minus

Query: 7 ttactataggcacgcgtggtcacggcccccggctg 42
||||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 11954 ttactataggcacgcgtggtcacggcccccggctg 11919

>gi|3643823|gb|AF075270.1|AF075270 Hordeum vulgare high affinity sulfate transporter (HVST1) gene,
promoter region, 5'UTR, and partial cds
Length = 1094

Score = 71.9 bits (36), Expect = 2e-09
Identities = 36/36 (100%)
Strand = Plus / Plus

Query: 7 ttactataggcacgcgtggtcacggcccccggctg 42
||||||| ||||| ||||| ||||| |||||
Sbjct: 64 ttactataggcacgcgtggtcacggcccccggctg 99

>gi|19919401|gb|AF435445.1| Pleurotus ostreatus manganese peroxidase (mnp3) gene, promoter
region and partial cds
Length = 2790

Score = 69.9 bits (35), Expect = 6e-09
Identities = 35/35 (100%)
Strand = Plus / Plus

Query: 8 tactataaggcacgcgtggtcacggcccccggctg 42
||||||| ||||| ||||| ||||| |||||
Sbjct: 79 tactataaggcacgcgtggtcacggcccccggctg 113

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>gi|8132114|gb|AF153014.1| Trichomonas vaginalis Tvp14 (tvp14) gene,
complete cds
Length = 1463

Score = 69.9 bits (35), Expect = 6e-09
Identities = 35/35 (100%)
Strand = Plus / Plus

Query: 8 tactatagggcacgcgtggtcgacggcccccggctg 42
|||||||
Sbjct: 11 tactatagggcacgcgtggtcgacggcccccggctg 45

>gi|4456992|gb|AF077743.1|AF077743 Mus musculus transcription factor TFEC
gene, promoter region and
5' UTR
Length = 615

Score = 69.9 bits (35), Expect = 6e-09
Identities = 38/39 (97%)
Strand = Plus / Plus

Query: 9 actataggcacgcgtggtcgacggcccccggctgttatt 47
|||||||
Sbjct: 1 actataaggcacgcgtggtcgacggcccccggctgttatt 39

>gi|12276207|gb|AF269146.1|AF269146 Bilophila wadsworthia taurine:pyruvate
aminotransferase gene,
complete cds
Length = 2050

Score = 69.9 bits (35), Expect = 6e-09
Identities = 35/35 (100%)
Strand = Plus / Minus

Query: 8 tactatagggcacgcgtggtcgacggcccccggctg 42
|||||||
Sbjct: 2050 tactatagggcacgcgtggtcgacggcccccggctg 2016

>gi|14275833|emb|AJ289605.1|MMU289605 Mus musculus partial Lancl1 gene
for LanC-like protein 1, exon 4
Length = 682

Score = 69.9 bits (35), Expect = 6e-09
Identities = 35/35 (100%)
Strand = Plus / Plus

Query: 9 actataaggcacgcgtggtcgacggcccccggctgt 43
|||||||
Sbjct: 1 actataaggcacgcgtggtcgacggcccccggctgt 35

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Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Plus

Query: 9 actataggcacgcgtggtcacggcccggtg 42
||||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 46 actataggcacgcgtggtcacggcccggtg 79

>gi|3378604|emb|AJ009889.1|HSAJ9889 Homo sapiens GHR gene, V1 promoter
region
Length = 1640

Score = 69.9 bits (35), Expect = 6e-09
Identities = 38/39 (97%)
Strand = Plus / Plus

Query: 9 actataggcacgcgtggtcacggcccggttatt 47
||||||| ||||| ||||| ||||| |||||
Sbjct: 1 actataaggcacgcgtggtcacggcccggttatt 39

>gi|3916231|gb|AF074397.1|AF074397 Homo sapiens anti-mullerian hormone type
II receptor (AMHR2)
gene, promoter region and partial cds
Length = 1135

Score = 69.9 bits (35), Expect = 6e-09
Identities = 38/39 (97%)
Strand = Plus / Plus

Query: 9 actataaggcacgcgtggtcacggcccggttatt 47
||||||| ||||| ||||| ||||| |||||
Sbjct: 13 actataaggcacgcgtggtcacggcccggttatt 51

>gi|5139506|emb|Z18892.2|MMDESMINP Mus musculus desmin gene
Length = 19391

Score = 69.9 bits (35), Expect = 6e-09
Identities = 35/35 (100%)
Strand = Plus / Minus

Query: 8 tactataaggcacgcgtggtcacggcccggtg 42
||||||| ||||| ||||| |||||
Sbjct: 19391 tactataaggcacgcgtggtcacggcccggtg 19357

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>gi|15487305|dbj|AB060299.1| Mus musculus gene for acetyl CoA synthethase-1, promoter region, partial sequence
Length = 2094

Score = 69.9 bits (35), Expect = 6e-09
Identities = 38/39 (97%)
Strand = Plus / Plus

Query: 9 actataggcacgcgtggtcacggcccggttatt 47
|||||||
Sbjct: 1 actataaggcacgcgtggtcacggcccggttatt 39

>gi|12697590|dbj|AB046716.1| Homo sapiens hST3Gal I gene for alpha 2,3-sialyltransferase I, promoter region
Length = 1950

Score = 69.9 bits (35), Expect = 6e-09
Identities = 38/39 (97%)
Strand = Plus / Plus

Query: 9 actataaggcacgcgtggtcacggcccggttatt 47
|||||||
Sbjct: 1 actataaggcacgcgtggtcacggcccggttatt 39

>gi|25453365|gb|AY050651.2| Giardia intestinalis MYB (MYB) mRNA, complete cds
Length = 3069

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Minus

Query: 9 actataaggcacgcgtggtcacggcccggtg 42
|||||||
Sbjct: 3069 actataaggcacgcgtggtcacggcccggtg 3036

Score = 52.0 bits (26), Expect = 0.001
Identities = 26/26 (100%)
Strand = Plus / Plus

Query: 17 gcacgcgtggtcacggcccggtg 42
|||||||
Sbjct: 1 gcacgcgtggtcacggcccggtg 26

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>gi|13183059|gb|AF237414.1| Anaplasma phagocytophilum RNA polymerase beta subunit (rpoB) gene,
complete cds
Length = 4185

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Minus

Query: 9 actataggcacgcgtggtcgacggcccggtg 42
|||||||
Sbjct: 4041 actataaggcacgcgtggtcgacggcccggtg 4008

>gi|13625520|gb|AY014277.1| Lolium perenne gibberellin 20-oxidase gene,
complete cds
Length = 2128

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Plus

Query: 9 actataaggcacgcgtggtcgacggcccggtg 42
|||||||
Sbjct: 15 actataaggcacgcgtggtcgacggcccggtg 48

>gi|17105179|gb|AF439558.1|AF439558 Mus musculus X2CR1 gene,, promoter
region and partial cds
Length = 830

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Plus

Query: 9 actataaggcacgcgtggtcgacggcccggtg 42
|||||||
Sbjct: 1 actataaggcacgcgtggtcgacggcccggtg 34

>gi|16209547|gb|AY052528.1| Glycine max calmodulin isoform-4 (cam-4) gene,
promoter region
and partial cds
Length = 2050

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Plus

Query: 5 gattactataaggcacgcgtggtcgacggcccg 38
|||||||
Sbjct: 13 gattactataaggcacgcgtggtcgacggcccg 46

16/21

>gi|15213480|gb|AF241535.1|AF241535 Homo sapiens mucin 4 (MUC4) gene, promoter sequence and partial
cds
Length = 3716

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Plus

Query: 9 actataggcacgcgtggtcgacggcccccggctg 42
|||||||
Sbjct: 1 actataaggcacgcgtggtcgacggcccccggctg 34

>gi|15558849|emb|AJ310936.1|FSO310936 Fusarium solani chy gene for putative cyanide hydratase enzyme
Length = 1981

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Minus

Query: 9 actataaggcacgcgtggtcgacggcccccggctg 42
|||||||
Sbjct: 1981 actataaggcacgcgtggtcgacggcccccggctg 1948

>gi|4878023|gb|AF131239.2|AF131239 Rattus norvegicus alpha 1,2-fucosyltransferase C (FTC) gene, complete
cds
Length = 1555

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Minus

Query: 9 actataaggcacgcgtggtcgacggcccccggctg 42
|||||||
Sbjct: 1534 actataaggcacgcgtggtcgacggcccccggctg 1501

>gi|15216031|emb|AJ318812.1|VFA318812 Vicia faba var. minor aapl gene, promoter region
Length = 1702

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Plus

Query: 9 actataaggcacgcgtggtcgacggcccccggctg 42
|||||||
Sbjct: 1 actataaggcacgcgtggtcgacggcccccggctg 34

17/21

>gi|4454294|emb|AJ132779.1|MMU132779 Mus musculus p107 gene promoter region
Length = 776

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Plus

Query: 9 actataggcacgcgtggtcgacggccggctg 42
|||||||
Sbjct: 1 actataaggcacgcgtggtcgacggccggctg 34

>gi|3133088|emb|Y16736.1|HSA16736 Homo sapiens dif-2 gene, promoter region
Length = 1368

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Plus

Query: 9 actataaggcacgcgtggtcgacggccggctg 42
|||||||
Sbjct: 11 actataaggcacgcgtggtcgacggccggctg 44

>gi|6690521|gb|AF154245.1|AF154245 Rattus norvegicus chemotactic protein-3
gene, complete cds
Length = 2416

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Plus

Query: 9 actataaggcacgcgtggtcgacggccggctg 42
|||||||
Sbjct: 1 actataaggcacgcgtggtcgacggccggctg 34

>gi|5731977|gb|AF114032.1|AF114032 Mus musculus glycogenin-1 gene,
promoter and partial cds
Length = 1958

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Plus

Query: 9 actataaggcacgcgtggtcgacggccggctg 42
|||||||
Sbjct: 1 actataaggcacgcgtggtcgacggccggctg 34

>gi|26453412|gb|AB094665.1| Seriola quinqueradiata YGHL1 gene for putative
growth hormone
like protein-1, complete cds
Length = 6658

18/21

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Plus

Query: 9 actataggcacgcgtggtcgacggcccggtg 42
|||||||
Sbjct: 39 actataggcacgcgtggtcgacggcccggtg 72

>gi|4039145|gb|AF099083.1|AF099083 Homo sapiens growth hormone secretagogue receptor gene, 5'
flanking region and partial cds
Length = 1237

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Plus

Query: 9 actataggcacgcgtggtcgacggcccggtg 42
|||||||
Sbjct: 1 actataggcacgcgtggtcgacggcccggtg 34

>gi|2739123|gb|AF029214.1|MMOX2S1 Mus musculus MRC OX-2 antigen homolog gene, exon 1
Length = 2791

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Minus

Query: 9 actataggcacgcgtggtcgacggcccggtg 42
|||||||
Sbjct: 2791 actataggcacgcgtggtcgacggcccggtg 2758

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Plus

Query: 9 actataggcacgcgtggtcgacggcccggtg 42
|||||||
Sbjct: 1 actataggcacgcgtggtcgacggcccggtg 34

>gi|2895903|gb|AF046916.1|AF046916 Ruminococcus flavefaciens FD-1 glutamine synthetase type III (glnA)
gene, complete cds
Length = 2685

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Minus

19/21

Query: 9 actataggcacgcgtggtcgacggcccggtg 42
 |||||||
Sbjct: 2685 actataggcacgcgtggtcgacggcccggtg 2652

Score = 58.0 bits (29), Expect = 2e-05
Identities = 29/29 (100%)
Strand = Plus / Plus

Query: 14 agggcacgcgtggtcgacggcccggtg 42
 |||||||
Sbjct: 1 agggcacgcgtggtcgacggcccggtg 29

>gi|1916583|gb|U53907.1|RNU53907 Rattus norvegicus microsatellite sequence
D10Mco29
Length = 498

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Plus

Query: 9 actataaggcacgcgtggtcgacggcccggtg 42
 |||||||
Sbjct: 5 actataaggcacgcgtggtcgacggcccggtg 38

>gi|6683556|dbj|AB024534.1| Rattus norvegicus gene for thiazide-sensitive
Na-Cl
cotransporter, 5' flanking region
Length = 2145.

Score = 67.9 bits (34), Expect = 2e-08
Identities = 34/34 (100%)
Strand = Plus / Plus

Query: 9 actataaggcacgcgtggtcgacggcccggtg 42
 |||||||
Sbjct: 1 actataaggcacgcgtggtcgacggcccggtg 34

>gi|7109286|gb|AF227508.1| Rattus norvegicus intestinal alkaline
phosphatase-II (IAP-II) gene,
complete cds
Length = 6359

Score = 65.9 bits (33), Expect = 1e-07
Identities = 33/33 (100%)
Strand = Plus / Minus

20/21

Query: 7 ttactataggcacgcgtggtcacggcccccggg 39
||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 6349 ttactataggcacgcgtggtcacggcccccggg 6317

>gi|13345792|gb|AF332759.1 Homo sapiens partially duplicated CHRNA7 gene, hybrid intron A/4 and partial exon 5 Length = 1280

Score = 65.9 bits (33), Expect = 1e-07
Identities = 36/37 (97%)
Strand = Plus / Plus

Query: 11 tataaggcacgcgtggtcacggcccccggctgttatt 47
||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 8 tataaggcacgcgtggtcacggcccccggctgttatt 44

>gi|5002511|emb|Z98266.1|HSZ98266 Homo sapiens gene encoding plakophilin (exons 1-13) Length = 49999

Score = 65.9 bits (33), Expect = 1e-07
Identities = 33/33 (100%)
Strand = Plus / Plus

Query: 10 ctataggcacgcgtggtcacggcccccggctg 42
||| ||| ||| ||| ||| ||| |||
Sbjct: 16 ctataggcacgcgtggtcacggcccccggctg 48

>gi|6560627|gb|AF112228.1|HSCD30P1 Homo sapiens CD30 protein (CD30) gene, promoter, partial sequence Length = 1605

Score = 65.9 bits (33), Expect = 1e-07
Identities = 37/39 (94%)
Strand = Plus / Plus

Query: 9 actataggcacgcgtggtcacggcccccggctgttatt 47
||| ||| ||| ||| ||| ||| |||
Sbjct: 1 actataggcacgcgtggtcacggccckggctggatt 39

>gi|24475537|dbj|AB084484.1| Betula platyphylla DNA, microsatellite:BpA Length = 427

Score = 65.9 bits (33), Expect = 1e-07
Identities = 33/33 (100%)
Strand = Plus / Minus

21/21

Query: 10 ctatagggcacgcgtggtcgacggcccggtg 42
|||||||
Sbjct: 317 ctatagggcacgcgtggtcgacggcccggtg 285

>gi|28875405|gb|AF515463.1| Biomphalaria glabrata fibrinogen related protein 12.1 precursor
(FREP12.1) gene, partial cds
Length = 609

Score = 63.9 bits (32), Expect = 4e-07
Identities = 32/32 (100%)
Strand = Plus / Plus

Query: 11 tatagggcacgcgtggtcgacggcccggtg 42
|||||||
Sbjct: 1 tatagggcacgcgtggtcgacggcccggtg 32

>gi|18140058|gb|AF457661.1| Castanea dentata clone ACS10A vascular protein gene, promoter
region
Length = 1157

Score = 63.9 bits (32), Expect = 4e-07
Identities = 35/36 (97%)
Strand = Plus / Plus

Query: 7 ttactatagggcacgcgtggtcgacggcccggtg 42
|||||||
Sbjct: 10 ttactatagggcacgcgtggtcgacggcccggtg 45

>gi|2581766|gb|U77633.1|RNU77633 Rattus norvegicus chromosome 10
microsatellite D10Mcc34
Length = 1023

Score = 63.9 bits (32), Expect = 4e-07
Identities = 33/34 (97%)
Strand = Plus / Minus

Query: 9 actatagggcacgcgtggtcgacggcccggtg 42
|||||||
Sbjct: 1023 actatagggcacgcgtggtcgacggcccggtg 990

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)